

What is claimed is:

1           1.     A computer-assisted method for generating predicted binding targets of  
2 a selected molecule, using a programmed computer including a processor, an input  
3 device, and an output device, including the steps of:

4           (a) inputting into the programmed computer, through the input device, data  
5 including the identity and three-dimensional coordinates of each of the atoms in the  
6 selected molecule;

7           (b) determining, using the processor, for each atom in the selected molecule, a  
8 predicted Gibbs free energy of binding of the atom to an ideal ligand for the atom;

9           (c) generating, using the processor, a three-dimensional prediction model of  
10 binding targets in the selected molecule by generating, using the three-dimensional  
11 coordinates of each of the atoms in the selected molecule, a model of the atoms in the  
12 selected molecule and mapping onto each atom depicted in the model the  
13 corresponding determined predicted Gibbs free energy of binding; and

14           (d) outputting, to the output device, the generated three-dimensional prediction  
15 model of binding targets.

1           2.     A computer-assisted method for predicting the binding affinity of a  
2 selected ligand for binding to a selected binding site of a selected molecule, using a  
3 programmed computer including a processor, an input device, and an output device,  
4 including the steps of:

5           (a) inputting into the programmed computer, through the input device, data  
6 including the identity and three-dimensional coordinates of each of the atoms in a  
7 selected binding site of a selected molecule;

8           (b) inputting into the programmed computer, through the input device, data  
9 including the identity and three-dimensional coordinates of each of the atoms in a  
10 selected compound;

11 (c) generating, using the processor, a model of the selected compound bound to  
12 the selected binding site;

13 (d) determining, using the processor, the three-dimensional coordinates of an  
14 energy minimized structure of the selected compound when the selected compound is  
15 bound to the selected binding site; and

16 (e) determining, using the processor, a predicted binding affinity of the energy  
17 minimized selected compound for the selected binding site.

1 3. A computer-assisted method for building a model of an ideal ligand for  
2 binding to a selected binding site of a selected molecule, using a programmed  
3 computer including a processor, an input device, and an output device, including the  
4 steps of:

5 (a) inputting into the programmed computer, through the input device, data  
6 including the identity and three-dimensional coordinates of each of the atoms in the  
7 selected binding site of the selected molecule;

8 (b) determining, using the processor, the identity and location of a set of ligand  
9 atoms that are energetically complementary to each of the atoms in the selected  
10 binding site of the selected molecule based on global optimization of the Gibbs energy  
11 of binding of each of the ligand atoms in the set of ligand atoms;

12 (c) generating, using the processor, a three-dimensional model of the set of  
13 ligand atoms bound to the selected binding site;

14 (d) outputting, to the output device, the three-dimensional model of the set of  
15 ligand atoms bound to the selected binding site.

1 4. A computer-assisted method for ranking each ligand in a set of selected  
2 ligands by its predicted binding affinities for binding to a selected binding site of a  
3 selected molecule, using a programmed computer including a processor, an input  
4 device, and an output device, including the steps of:

5 (a) inputting into the programmed computer, through the input device, data  
6 including, the identity and three-dimensional coordinates of each of the atoms in a  
7 selected binding site of a selected molecule;

8 (b) determining the predicted binding affinity of each ligand in the set of  
9 ligands to the selected binding site of the selected molecule by:

10 (i) inputting into the programmed computer, through the input device,  
11 data including the identity and three-dimensional coordinates of each of  
12 the atoms in the selected compound;

13 (ii) generating, using the processor, a model of the selected compound  
14 bound to the selected binding site;

15 (iii) determining, using the processor, the three-dimensional coordinates  
16 of an energy minimized structure of the selected compound when the  
17 selected compound is bound to the selected binding site; and

18 (iv) determining, using the processor, a predicted binding affinity of the  
19 energy minimized selected compound for the selected binding site; and

20 (b) ranking each ligand according to its determined predicted binding affinity.

1 5. A computer-assisted method for generating predicted binding targets on  
2 a internal, non-solvent exposed surface of a selected molecule, using a programmed  
3 computer including a processor, an input device, and an output device, including the  
4 steps of:

5 (a) inputting into the programmed computer, through the input device, data  
6 including the identity and three-dimensional coordinates of each of the atoms in a  
7 selected partially unfolded state of the selected molecule, the selected partially folded  
8 state including a folded portion and an unfolded portion;

9 (b) determining, using the processor, for each atom in the folded portion of the  
10 selected partially unfolded state of the selected molecule, a predicted Gibbs free energy  
11 of binding of the atom to the ideal ligand for the atom;

12 (c) generating, using the processor, a three-dimensional prediction model of  
13 binding targets in the folded portion of the selected partially unfolded state of the  
14 selected molecule by generating, using the three-dimensional coordinates of each of the  
15 atoms in the folded portion of the selected partially unfolded state of the selected  
16 molecule, a model of the atoms in the folded portion of the selected partially unfolded  
17 state of the selected molecule and mapping onto each atom depicted in the model the  
18 corresponding determined predicted Gibbs free energy of binding; and  
19 (d) outputting, to the output device, the generated three-dimensional prediction  
20 model of binding targets.

1 6. A computer-assisted method for predicting the binding affinity of a  
2 selected peptide ligand for binding to a selected binding site of a selected molecule,  
3 using a programmed computer including a processor, an input device, and an output  
4 device, including the steps of:  
5 (a) inputting into the programmed computer, through the input device, data  
6 including the identity and three-dimensional coordinates of each of the atoms in a  
7 selected binding site of a selected molecule;  
8 (b) inputting into the programmed computer, through the input device, data  
9 including, the identity and three-dimensional coordinates of each of the atoms in a  
10 selected dipeptide;  
11 (c) generating, using the processor, a model of the selected dipeptide bound to  
12 the selected binding site;  
13 (d) determining, using the processor, the three-dimensional coordinates of an  
14 energy minimized structure of the selected dipeptide when the selected dipeptide is  
15 bound to the selected binding site; and  
16 (e) determining, using the processor, a predicted binding affinity of the energy  
17 minimized dipeptide for the selected binding site.

1           7.     The method of claim 6, further including:  
2           repeating steps (a) - (e) for a plurality of selected dipeptides and identifying as  
3     a lead dipeptide the selected dipeptide having the highest determined binding affinity.

1           8.     The method of claim 2, further including:  
2           (f) selecting a first polypeptide of three or more amino acids, the polypeptide  
3     including the dipeptide;  
4           (g) generating, using the processor, a model of the selected first polypeptide  
5     bound to the selected binding site;  
6           (h) determining, using the processor, the three-dimensional coordinates of an  
7     energy minimized structure of the selected first polypeptide when the selected first  
8     polypeptide is bound to the selected binding site; and  
9           (i) determining, using the processor, a predicted binding affinity of the energy  
10    minimized first polypeptide for the selected binding site.

1           9.     The method of claim 8, further including:  
2           (j) selecting a second polypeptide including the first polypeptide;  
3           (k) generating, using the processor, a model of the selected second polypeptide  
4     bound to the selected binding site;  
5           (l) determining, using the processor, the three-dimensional coordinates of an  
6     energy minimized structure of the selected second polypeptide when the second  
7     selected polypeptide is bound to the selected binding site; and  
8           (m) determining, using the processor, a predicted binding affinity of the energy  
9     minimized second polypeptide for the selected binding site.

1           10.    The method of claim 8, further including:  
2           (j) selecting a variant of the selected polypeptide;  
3           (k) generating, using the processor, a model of the selected variant polypeptide  
4 bound to the selected binding site;  
5           (l) determining, using the processor, the three-dimensional coordinates of an  
6 energy minimized structure of the selected variant polypeptide when the selected  
7 variant polypeptide is bound to the selected binding site; and  
8           (m) determining, using the processor, a predicted binding affinity of the energy  
9 minimized selected variant polypeptide for the selected binding site.

1           11.    The method of claim 5 wherein the selected partially unfolded state is  
2 the partially unfolded state having the lowest Gibbs energy of any potential partially  
3 unfolded state of the selected molecule.

1           ~~12.~~   A computer program, residing on a computer-readable medium, for  
2 generating predicted binding targets of a selected molecule, the computer program  
3 including instructions for causing a computer to:  
4           (a) receive data including the identity and three-dimensional coordinates of each  
5 of the atoms in the selected molecule;  
6           (b) determine, for each atom in the selected molecule, a predicted Gibbs free  
7 energy of binding of the atom to an ideal ligand for the atom;  
8           (c) generate a three-dimensional prediction model of binding targets in the  
9 selected molecule by generating, using the three-dimensional coordinates of each of the  
10 atoms in the selected molecule, a model of the atoms in the selected molecule and  
11 mapping onto each atom depicted in the model the corresponding determined predicted  
12 Gibbs free energy of binding; and  
13           (d) output the generated three-dimensional prediction model of binding targets.

1 13. A computer program, residing on a computer-readable medium, for  
2 predicting the binding affinity of a selected ligand for binding to a selected binding  
3 site of a selected molecule, the computer program including instructions for causing  
4 a computer to:

5 (a) receive data including the identity and three-dimensional coordinates of each  
6 of the atoms in a selected binding site of a selected molecule;

7 (b) receive data including the identity and three-dimensional coordinates of  
8 each of the atoms in a selected compound;

9 (c) generate a model of the selected compound bound to the selected binding  
10 site;

11 (d) determine the three-dimensional coordinates of an energy minimized  
12 structure of the selected compound when the selected compound is bound to the  
13 selected binding site; and

14 (e) determine a predicted binding affinity of the energy minimized selected  
15 compound for the selected binding site.

1 14. A computer program, residing on a computer-readable medium, for  
2 building a model of an ideal ligand for binding to a selected binding site of a selected  
3 molecule, the computer program including instructions for causing a computer to:

4 (a) receive data including the identity and three-dimensional coordinates of  
5 each of the atoms in the selected binding site of the selected molecule;

6 (b) determine the identity and location of a set of ligand atoms that are  
7 energetically complementary to each of the atoms in the selected binding site of the  
8 selected molecule based on global optimization of the Gibbs energy of binding of each  
9 of the ligand atoms in the set of ligand atoms;

10 (c) generate a three-dimensional model of the set of ligand atoms bound to the  
11 selected binding site; and

12 (d) output the three-dimensional model of the set of ligand atoms bound to the

13 selected binding site.

1 15. A computer program, residing on a computer-readable medium, for  
2 ranking each ligand in a set of selected ligands by its predicted binding affinities for  
3 binding to a selected binding site of a selected molecule, the computer program  
4 including instructions for causing a computer to:

5 (a) receive data including the identity and three-dimensional coordinates of  
6 each of the atoms in a selected binding site of a selected molecule;

7 (b) determine the predicted binding affinity of each ligand in the set of ligands  
8 to the selected binding site of the selected molecule by:

9 (i) receiving data including the identity and three-dimensional  
10 coordinates of each of the atoms in the selected compound;

11 (ii) generating a model of the selected compound  
12 bound to the selected binding site;

13 (iii) determining the three-dimensional coordinates  
14 of an energy minimized structure of the selected compound when the  
15 selected compound is bound to the selected binding site; and

16 (iv) determining a predicted binding affinity of the  
17 energy minimized selected compound for the selected binding site;

18 (b) rank each ligand according to its determined predicted binding affinity.

1 16. A computer program, residing on a computer-readable medium, for  
2 generating predicted binding targets on a internal, non-solvent exposed surface of a  
3 selected molecule, the computer program including instructions for causing a computer  
4 to:

5 (a) receive data including the identity and three-dimensional coordinates of each  
6 of the atoms in a selected partially unfolded state of the selected molecule, the selected  
7 partially unfolded state including a folded portion and an unfolded portion;



8 (b) determine, for each atom in the folded portion of the selected partially  
9 unfolded state of the selected molecule, a predicted Gibbs free energy of binding of  
10 the atom to the ideal ligand for the atom;

11 (c) generate a three-dimensional prediction model of binding targets in the  
12 folded portion of the selected partially unfolded state of the selected molecule by  
13 generating, using the three-dimensional coordinates of each of the atoms in the folded  
14 portion of the selected partially unfolded state of the selected molecule, a model of the  
15 atoms in the folded portion of the selected partially unfolded state of the selected  
16 molecule and mapping onto each atom depicted in the model the corresponding  
17 determined predicted Gibbs free energy of binding; and

18 (d) output the generated three-dimensional prediction  
19 model of binding targets.

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1 17. A computer program, residing on a computer-readable medium, for  
2 predicting the binding affinity of a selected peptide ligand for binding to a selected  
3 binding site of a selected molecule, the computer program comprising instructions for  
4 causing a computer to:

5 (a) receive data including the identity and three-dimensional coordinates of each  
6 of the atoms in a selected binding site of a selected molecule;

7 (b) receive data including, the identity and three-dimensional coordinates of  
8 each of the atoms in a selected dipeptide;

9 (c) generate a model of the selected dipeptide bound to the selected binding  
10 site;

11 (d) determine the three-dimensional coordinates of an energy minimized  
12 structure of the selected dipeptide when the selected dipeptide is bound to the selected  
13 binding site; and

14 (e) determine a predicted binding affinity of the energy minimized dipeptide for  
15 the selected binding site.